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Scientific Letters

Poster 9

Epidemiology and discrimination of clinically relevant *Enterobacter cloacae* complex species in Northern Portugal

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Abstract

Background: *E. cloacae* complex species are increasingly implicated in infections caused by multidrug-resistant bacteria, but their epidemiology is scarce due to the limitations of automated methods in accurate species identification (e.g. VITEK2/ MALDI–TOF MS) [1]. FT-IR is a promising quick, simple and low-cost alternative for bacterial discrimination [2]. **Objective:** We aim to assess the epidemiology of *Enterobacter* spp. isolates causing infections in two hospitals from North of Portugal, and the potential of FT-IR to differentiate the main clinically relevant *Enterobacter* species. **Methods:** We analyzed forty-five *Enterobacter* isolates from infection (*n*=43) or colonization (*n*=2) identified between 2019-2021 by VI-TEK2. Species identification was confirmed by PCR and sequencing of *hsp60*, used to build a phylogenetic tree with MEGA7 software. Antibiotic susceptibility testing was performed by standard methods according to EUCAST. Spectra from the most frequent species were acquired in the ATR mode of FT-IR equipment (Spectrum Two, Perkin-Elmer) in standardized conditions (4000-400cm-1; 4cm-1 resolution), processed (SNV, Saviztky-Golay) and used to identify species discriminatory profiles using PLSDA with Clover MS Data Analysis software, as described [3]. **Results:** Only 73% of the isolates were *Enterobacter* identified as *E. hormaechei* (*n*=19), *E. kobei* (*n*=7), *E. asburiae* (*n*=3), *E. bugandensis* (*n*=2), *E. cloacae* (*n*=1) and *E. ludwigii* (*n*=1). A few isolates produced VIM-1 (*E. hormaechei*), KPC (*E. cloacae*) or ESBL (4 species) The remaining isolates were identified as *K. aerogenes* (*n*=7), *K. variicola* (*n*=3), *E. coli* (*n*=1) and *K. michiganensis* (*n*=1). By using a PLSDA model, we were able to discriminate *E. kobei* and *E. hormaechei* with 92% average correct predictions. **Conclusions:** We found that *E. hormaechei* and *E. kobei* are the most frequent species causing hospital infections and that FT-IR can accurately differentiate these species, opening the possibility for its expansion to other *E. cloacae* complex species.

Keywords: bacterial identification; *Enterobacter* spp.; FT-IR spectroscopy

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